SEQUENCE LISTING

- <110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.
 Kazusa DNA Research Institute
- <120> Novel gene encoding brain-specific membrane protein
- <130> C2-010PCT
- <150> JP 1998-331727
- <151> 1998-11-20
- <160> 7
- ⟨210⟩ 1
- <211> 3144
- <212> DNA
- <213> Homo sapiens
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ctttaatctg	gaagagaaga	gaacaagttg	tgcttttccc	cccttcttct tgctaaacgc	240
catggatata	actgaataag	cggctcaggg	ctttccccgc	gtggacgtcc gaggccacca	300
tctgcctgca	ttcgccggag	ccgccggagg	gtttagctcg	agtctgtctc gggcggggaa	360
ggatgcgtgg	ccgagccggg	gagcccgggc	gccccgcgga	gccggcctcg gtgccaccca	420
gccgggggta	gatgctgcct	cgcccaggcg	ctgagtgacc	agacc atg gag acc ctg Met Glu Thr Leu	477
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				gcc gtg gtc gac gcc	525
Leu Gly Gly		la Phe Gly 1 10	Met Ala Phe	Ala Val Val Asp Ala 20	
tgo coc aas	z tac tet e	to tgo cag :	aat ctø tet	gag toa otg ggg acc	573

25

Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr

30

ctg	tgc	ccc	tcc	aag	ggg	ctg	ctc	ttt	gta	ccc	cct	gat	att	gac	cgg	621
Leu	Cys	Pro	Ser	Lys	Gly	Leu	Leu	Phe	Val	Pro	Pro	Asp	Ile	Asp	Arg	
			40					45					50			
cgg	aca	gtg	gag	ctg	cgc	ctg	ggc	ggc	aac	ttc	atc	atc	cac	atc	agc	669
Arg	Thr	Val	Glu	Leu	Arg	Leu	Gly	Gly	Asn	Phe	Ile	Ile	His	Ile	Ser	
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Arg	G1n	Asp	Phe	Ala	Asn	Met	Thr	Gly	Leu	Val	Asp	Leu	Thr	Leu	Ser	
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agg	aac	acc	atc	agc	cac	atc	cag	ccc	ttt	tcc	ttt	ctg	gac	ctc	gag	765
Arg	Asn	Thr	Ile	Ser	His	Ile	Gln	Pro	Phe	Ser	Phe	Leu	Asp	Leu	Glu	
85					90					95					100	
agc	ctc	cgc	tcc	ctg	cat	ctt	gac	agc	aat	cgg	ctg	cca	agc	ctt	ggg	813
Ser	Leu	Arg	Ser	Leu	His	Leu	Asp	Ser	Asn	Arg	Leu	Pro	Ser	Leu	Gly	
				105					110					115		
gag	gac	acc	ctc	cgg	ggc	ctg	gtc	aac	ctg	cag	cac	ctt	atc	gtg	aac	861
Glu	Asp	Thr	Leu	Arg	G1y	Leu	Val	Asn	Leu	Gln	His	Leu	Ile	Val	Asn	
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aac aac cag ctg ggc ggc atc gca gat gag gct ttt gag gac ttc ctg

Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu

135
140
145

ctg aca ttg gag gat ctg gac ctc tcc tac aac aac ctc cat ggc ctg 957

Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu

150 155 160

ccg tgg gac tcc gtg cga cgc atg gtc aac ctc cac cag ctg agc ctg1005Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu175180

gac cac aac ctg ctg gat cac atc gcc gag ggc acc ttt gca gac ctg 1053
Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu
185 190 195

cag aaa ctg gcc cgc ctg gat ctc acc tcc aat cgg ctg cag aag ctg 1101

Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu

200 205 210

ccc cct gat ccc atc ttt gcc cgc tcc cag gct tcg gct ttg aca gcc 1149

Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala
215 220 225

aca ccc ttt gcc cca ccc ttg tcc ttt agt ttt ggg ggt aac cca ctt 1197

Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu

230 235 240

Cac	tgc	aat	ıgı	gag	CLL	CLC	rgg	CLg	cgg	agg	CLC	gag	cgg	gac	gaı	1245
His	Cys	Asn	Cys	Glu	Leu	Leu	Trp	Leu	Arg	Arg	Leu	Glu	Arg	Asp	Asp	
245					250					255					260	
gac	ctg	gaa	acc	tgt	ggc	tcc	cca	ggg	ggc	ctc	aag	ggt	cgc	tac	ttc	1293
Asp	Leu	Glu	Thr	Cys	Gly	Ser	Pro	Gly	Gly	Leu	Lys	Gly	Arg	Tyr	Phe	
				265					270					275		
tgg	cat	gtg	cgt	gag	gag	gag	ttt	gtg	tgc	gag	ccg	cct	ctc	atc	acc	1341
Trp	His	Val	Arg	Glu	Glu	Glu	Phe	Val	Cys	Glu	Pro	Pro	Leu	Ile	Thr	
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cag	cac	aca	cac	aag	ttg	ctg	gtt	ctg	gag	ggc	cag	gcg	gcc	aca	ctc	1389
					Leu											
0111		295		2,0	Lou	Dou	300	Dou	014	01)	0111	305	71.10	1111	Bou	
		230					300					303				
																1.407
					ggg											1437
Lys	Cys	Lys	Ala	Ile	Gly	Asp	Pro	Ser	Pro	Leu	Ile	His	Trp	Val	Ala	
	310					315					320					
ccc	gat	gac	cgc	ctg	gta	ggg	aac	tcc	tca	agg	acc	gct	gtc	tat	gac	1485
Pro	Asp	Asp	Arg	Leu	Val	Gly	Asn	Ser	Ser	Arg	Thr	Ala	Val	Tyr	Asp	
325					330					335					340	
aat	ggc	acc	ctg	gac	atc	ttc	atc	acc	aca	tct	cag	gac	agt	ggt	gcc	1533

Asn	Gly	Thr	Leu	Asp	Ile	Phe	Ile	Thr	Thr	Ser	Gln	Asp	Ser	Gly	Ala	
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ttc	acc	tgc	att	gct	gcc	aat	gct	gcc	gga	gag	gcc	acg	gcc	atg	gtg	1581
Phe	Thr	Cys	Ile	Ala	Ala	Asn	Ala	Ala	Gly	Glu	Ala	Thr	Ala	Met	Val	
			360					365					370			
gag	gtc	tcc	atc	gtc	cag	ctg	cca	cac	ctc	agc	aac	agc	acc	agc	cgc	1629
Glu	Val	Ser	Ile	Val	Gln	Leu	Pro	His	Leu	Ser	Asn	Ser	Thr	Ser	Arg	
		375					380					385				
act	gca	ccc	ccc	aag	tcc	cgc	ctc	tca	gac	atc	act	ggc	tcc	agc	aag	1677
Thr	Ala	Pro	Pro	Lys	Ser	Arg	Leu	Ser	Asp	Ile	Thr	Gly	Ser	Ser	Lys	
	390					395					400					
acc	agc	cgg	gga	ggt	gga	ggc	agt	ggg	ggc	gga	gag	cct	ссс	aaa	agc	1725
Thr	Ser	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Glu	Pro	Pro	Lys	Ser	
405					410					415					420	
ccc	ccg	gaa	cgg	gct	gtg	ctt	gtg	tct	gaa	gtg	acc	acc	acc	tcg	gcc	1773
Pro	Pro	Glu	Arg	Ala	Val	Leu	Val	Ser	Glu	Val	Thr	Thr	Thr	Ser	Ala	
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440 445 450

1821

ctg gtc aag tgg tct gtc agc aag tca gca ccc cgg gtg aag atg tac

Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr

cag	ctg	cag	tac	aac	tgc	tct	gac	gat	gag	gta	ctg	att	tac	agg	atg	1869
Gln	Leu	Gln	Tyr	Asn	Cys	Ser	Asp	Asp	Glu	Val	Leu	Ile	Tyr	Arg	Met	
		455					460					465				
atc	cca	gcc	tcc	aac	aag	gcc	ttc	gtg	gtc	aac	aac	ctg	gtg	tca	ggg	1917
Ile	Pro	Ala	Ser	Asn	Lys	Ala	Phe	Val	Val	Asn	Asn	Leu	Val	Ser	Gly	
	470					475					480					
act	ggc	tac	gac	ttg	tgt	gtg	ctg	gcc	atg	tgg	gat	gac	aca	gcc	acg	1965
Thr	Gly	Tyr	Asp	Leu	Cys	Val	Leu	Ala	Met	Trp	Asp	Asp	Thr	Ala	Thr	
485					490					495					500	
aca	ctc	acg	gcc	acc	aac	atc	gtg	ggc	tgc	gcc	cag	ttc	ttc	acc	aag	2013
Thr	Leu	Thr	Ala	Thr	Asn	Ile	Val	Gly	Cys	Ala	Gln	Phe	Phe	Thr	Lys	
				505					510					515		
gct	gac	tac	ccg	cag	tgc	cag	tcc	atg	cac	agc	cag	att	ctg	ggc	ggc	2061
Ala	Asp	Tyr	Pro	G1n	Cys	Gln	Ser	Met	His	Ser	Gln	Ile	Leu	Gly	Gly	
			520					525					530			
acc	atg	atc	ctg	gtc	atc	ggg	ggc	atc	atc	gtg	gcc	acg	ctg	ctg	gtc	2109
Thr	Met	Ile	Leu	Val	Ile	G1y	Gly	Ile	Ile	Val	Ala	Thr	Leu	Leu	Val	
		535					540					545				

ttc atc gtc atc ctc atg gtg cgc tac aag gtc tgc aac cac gag gcc

Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala 550 555 560

ccc agc aag atg gca gcg gcc gtg agc aat gtg tac tcg cag acc aac 2205
Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn
565 570 575 580

cag ggc ccg ccg aag gtg gtg gtg cgc aac gag ctc ctg gac ttc acc 2301

Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr

600 605 610

gcc agc ctg gcc cgc gcc agt gac tcc tct tcc tcc agc tcc ctg ggc 2349

Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly

615 620 625

agt ggg gag gct gcg ggg ctg gga cgg gcc ccc tgg agg atc cca ccc 2397

Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro
630 635 640

tcc gcc ccg cgc ccc aag ccc agc ctt gac cgc ctg atg ggg gcc ttc

2445

Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe

645

650

655

660

gcc	tcc	ctg	gac	ctc	aag	agt	cag	aga	aag	gag	gag	ctg	ctg	gac	tcc	2493
Ala	Ser	Leu	Asp	Leu	Lys	Ser	Gln	Arg	Lys	Glu	Glu	Leu	Leu	Asp	Ser	
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agg	act	cca	gcc	ggg	aga	ggg	gct	ggg	acg	tcg	gcc	cgg	ggc	cac	cac	2541
Arg	Thr	Pro	Ala	Gly	Arg	Gly	Ala	Gly	Thr	Ser	Ala	Arg	Gly	His	His	
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Ser	Asp	Arg	Glu	Pro	Leu	Leu	G1y	Pro	Pro	Ala	Ala	Arg	Ala	Arg	Ser	
		695					700					705				
ctg	ctc	ссс	ttg	ccg	ttg	gag	ggc	aag	gcc	aaa	cgc	agc	cac	tcc	ttc	2637
Leu	Leu	Pro	Leu	Pro	Leu	Glu	Gly	Lys	Ala	Lys	Arg	Ser	His	Ser	Phe	
	710					715					720					
gac	atg	ggg	gac	ttt	gct	gct	gcg	gcg	gcg	gga	ggg	gtc	gtg	ccg	ggc	2685
Asp	Met	Gly	Asp	Phe	Ala	Ala	Ala	Ala	Ala	Gly	Gly	Val	Val	Pro	Gly	
725					730					735					740	
ggc	tac	agt	cct	cct	cgg	aag	gtc	tcg	aac	atc	tgg	acg	aag	cgc	agc	2733
Gly	Tyr	Ser	Pro	Pro	Arg	Lys	Val	Ser	Asn	Ile	Trp	Thr	Lys	Arg	Ser	
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ctc tct gtc aac ggc atg ctc ttg ccc ttt gag gag agt gac ctg gtg

Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val
760 765 770

ggg	gcc	cgg	ggg	act	ttt	ggc	agc	tcc	gaa	tgg	gtg	atg	gag	agc	acg	2829
Gly	Ala	Arg	Gly	Thr	Phe	Gly	Ser	Ser	Glu	Trp	Val	Met	Glu	Ser	Thr	
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gtc taggtggggg tgggcatgct ccctttcctg tgcgcagggt gggagaaggg 2882
Val

gaaagaatct cactggcaag tgtttgtgga gtttccatgg tgatgtttac atccagggac 2942

agtttcgtct ccctgtcaat ggcctcgtgt cccccctac cccgcaacac ccacatcacc 3002

tccccaccac ccggccgggg tgtgctcagg gaatgtggac tcgctcaaat gccggactga 3062

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25 30 35

Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg
40 45 50

Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser
55 60 65

Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser
70 75 80

Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu 85 90 95 100

Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly
105 110 115

Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn
120 125 130

Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu
135 140 145

Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu
150 155 160

Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu
165 170 175 180

Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu
185 190 195

Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu
200 205 210

Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala 215 220 225

Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu 230 235 240

His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp 245 250 255 260

Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe
265 270 275

Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr
280 285 290

Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu
295 300 305

Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala 310 315 320

Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp
325 330 335 340

Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala

345

350

355

Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val

Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg 375 380 385

Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys

C.)

390 395 400

Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu Pro Pro Lys Ser 405 410 415 420

Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala
425 430 435

Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr
440 445 450

Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met
455 460 465

Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly
470 475 480

Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr
485 490 495 500

Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys

505 510 515

Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly
520 525 530

Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val
535 540 545

Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala 550 555 560

Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn 565 570 575 580

Gly Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro 585 590 595

Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr
600 605 610

Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Leu Gly
615 620 625

Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro 630 635 640

Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe 645 650 655 660

Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser

665 670 675

Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His
680 685 690

Ser Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser
695 700 705

Leu Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe
710 715 720

Asp Met Gly Asp Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro Gly
725 730 735 740

Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser

745

750

755

Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val
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Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr
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Val

<212> DNA

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